

Appendix II

Alignment of instant SEQ ID NO: 1 with SEQ ID NO: 1479 of Tang et al.

<!--StartFragment-->RESULT 2

AAM78817

ID AAM78817 standard; protein; 956 AA.

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AC AAM78817;

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DT 06-NOV-2001 (first entry)

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DE Human protein SEQ ID NO 1479.

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KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;

KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;

KW tissue growth factor; immunomodulatory; cancer; leukaemia;

KW nervous system disorder; arthritis; inflammation.

XX

OS Homo sapiens.

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PN WO200157190-A2.

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PD 09-AUG-2001.

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PF 05-FEB-2001; 2001WO-US004098.

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PR 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00560875.

PR 20-JUN-2000; 2000US-00598075.

PR 19-JUL-2000; 2000US-00620325.

PR 01-SEP-2000; 2000US-00654936.

PR 15-SEP-2000; 2000US-00663561.

PR 20-OCT-2000; 2000US-00693325.

PR 30-NOV-2000; 2000US-00728422.

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PA (HYSE-) HYSEQ INC.

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PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;

PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;

PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

XX

DR WPI; 2001-476283/51.

DR N-PSDB; AAK51950.

XX

PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.

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FS Claim 20; Page 3755-3757; 6221pp; English.

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CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication

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SQ Sequence 956 AA;

Query Match		99.9%;	Score 4990;	DB 4;	Length 956;	
Best Local Similarity		99.9%;	Pred. No. 0;			
Matches 955;		Conservative	1;	Mismatches	0;	Indels 0; Gaps 0;
Qy	1	MASKRRKSTTPCMIPVKTVVLQDASMEAQPAETLPEGPQQDLPEEASASSEAQNPSSTD	60			
Db	1	MASKRRKSTTPCMIPVKTVVLQDASMEAQPAETLPEGPQQDLPEEASASSEAQNPSSTD	60			
Qy	61	GSTLANGHRSTLDGGLYSCKYCDFRSHDMTQFVGHMNSHEDFNKDPFTFVCSGCFLAKT	120			
Db	61	GSTLANGHRSTLDGGLYSCKYCDFRSHDMTQFVGHMNSHEDFNKDPFTFVCSGCFLAKT	120			
Qy	121	PEGLSLHNATCHSGEASFVWNVAKPDNHVVVEQSIPESTSTPDLAGEPSAEGADGQAEII	180			
Db	121	PEGLSLHNATCHSGEASFVWNVAKPDNHVVVEQSIPESTSTPDLAGEPSAEGADGQAEII	180			
Qy	181	ITKTPIMKIMKGAEAKKIHTLKENVPSQPVGEALPKLSTGEMEVREGDHSFINGAVPVS	240			
Db	181	ITKTPIMKIMKGAEAKKIHTLKENVPSQPVGEALPKLSTGEMEVREGDHSFINGAVPVS	240			
Qy	241	QASASSAKNPHAANGPLIGTVPVLPAGIAQFLSLQQQPPVHAQHVVHQPLPTAKALPKVM	300			
Db	241	QASASSAKNPHAANGPLIGTVPVLPAGIAQFLSLQQQPPVHAQHVVHQPLPTAKALPKVM	300			
Qy	301	IPLSSIPTYNAAAMDNSFLKNSFHKKFPYPTKAELCYLTVVTKYPEEQLKIWFTAQRLKQG	360			
Db	301	IPLSSIPTYNAAAMDNSFLKNSFHKKFPYPTKAELCYLTVVTKYPEEQLKIWFTAQRLKQG	360			
Qy	361	ISWSPEEIEDARKKMFNTVIQSVQPQTTITVLNTPLVASAGNVQHLIQAALPGHVVGQPEG	420			
Db	361	ISWSPEEIEDARKKMFNTVIQSVQPQTTITVLNTPLVASAGNVQHLIQAALPGHVVGQPEG	420			
Qy	421	TGGGLLVTPQLMANGLIQATSSPLPLTVTSVPKQPGVAPINTVCSNTTSVAVKVVNAAQSLL	480			
Db	421	TGGGLLVTPQLMANGLIQATSSPLPLTVTSVPKQPGVAPINTVCSNTTSVAVKVVNAAQSLL	480			
Qy	481	TACPSITSQAFLDASIYKNKKSHEQLSALKGSCFRNQFPQGSEVEHLTKVTGLSTREVRK	540			
Db	481	TACPSITSQAFLDASIYKNKKSHEQLSALKGSCFRNQFPQGSEVEHLTKVTGLSTREVRK	540			
Qy	541	WFSRRRYHCRNLKGSRAMIPGDHSSIIIDSVPESVSPSSKVPVETCIPTTATLATHPSA	600			
Db	541	WFSRRRYHCRNLKGSRAMIPGDHSSIIIDSVPESVSPSSKVPVETCIPTTATLATHPSA	600			
Qy	601	KRQSWHQTPDFPTTKYKERAPEQLRALESSFAQNPLPLDEELDRLRSETKMTREIDSWF	660			
Db	601	KRQSWHQTPDFPTTKYKERAPEQLRALESSFAQNPLPLDEELDRLRSETKMTREIDSWF	660			
Qy	661	SERRKKVNAEETKKAENASQEEEEAAEDEGGEEDLASELRVSGENGSEMPSSHILAER	720			
Db	661	SERRKKVNAEETKKAENASQEEEEAAEDEGGEEDLASELRVSGENGSEMPSSHILAER	720			
Qy	721	KVSPPIKINLKNLRVTEANGRNEIPGLGACDPEDDESINKLAEQLPGKVSCKTKAQQRHLR	780			
Db	721	KVSPPIKINLKNLRVTEANGRNEIPGLGACDPEDDESINKLAEQLPGKVSCKTKAQQRHLR	780			
Qy	781	QLFVQQTQWPSNQDYDSIMAQTGLPRPEVVRWFGDSRYALKNGQLKWYEDYKRGNFPPGLL	840			
Db	781	QLFVQQTQWPSNQDYDSIMAQTGLPRPEVVRWFGDSRYALKNGQLKWYEDYKRGNFPPGLL	840			

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Qy      841  VIAPGNRELLQDYIMTHKMLYEEDLQNLCDKTQMSSQQVKQWFAEKMGEETRAVADTGSE 900
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841  VIAPGNRELLQDYIMTHKMLYEEDLQNLCDKTQMSSQQVKQWFAEKMGEETRAVADTGSE 900
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      901  DQGPGTGELTAVHKGMGDTYSEVSENSESWEPRVPEASSEPFDTSPPQAGRQLETD 956
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901  DQGPGTGELTAVHKGMGDTYSEVSENSESWEPRVPEASSEPFDTSPPQAGRQLETD 956
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